SEQUENCE LISTING

<110> King, Kendall W Madura, Rebecca A Rosey, Everett L

<120> NUCLEIC ACIDS AND PROTIINS OF THE MYCOPLASMA PNEUMONIAE mhp3 GENE AND USES THEREOF

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<140> PC10555

<141> 1999-09-29

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<170> PatentIn Ver. 2.1

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Thr Asp Val Ser Lys Ile Ser Gly Leu Val Asn Glu Arg Lys Ser Glu
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Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Gly Glu 100 105 110

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His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln 145 150 155 160

Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp 165 170 175

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 - Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu 225 230 235 240
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 - Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp 260 265 270
 - Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro 275 280 285
 - Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu Ile Phe Ser Asp 290 295 300
 - Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly Val Asp Thr Asp 305 310 315 320
 - Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe Phe Thr Ser Ile , 325 330 335
 - Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu Ser Asp Leu Tyr 340 345 350
 - Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe Glu Phe Gly Lys 355 360 365
 - Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg Phe Val Asp Ile 370 375 380
 - Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu Ala Thr Glu Ala 385 390 395 400
 - Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr Lys Thr Ile Pro
 405 410 415
 - Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu Met Pro Asp Lys
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manipulated for in vitro expression

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Arg	Lys	Ser 35	Glu	Ile	Met	Ala	Ala 40		Ala	Asp	Ala	Asn 45	Lys	His	Phe
Gly	Leu 50	Asn	Met	Ala	Ile	Val 55	Thr	Ala	Gly	Gly	Thr 60	Val	Asn	Asp	Asn
Ser 65	Phe	Asn	Gln	Ser	Gly 70	Trp	Glu	Ala	Ile	Gln 75	Gln	Leu	Gly	Ala	80
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Gly	Lys	Tyr	Ser 100	Ser	Leu	Ala	Asn	Thr 105	Asn	Lys	Asn	Val	Trp 110	Val	Leu
Ser	Gly	Phe 115	Gln	His	Gly	Asp	Ala 120	Phe	Thr	Arg	Trp	Leu 125	Lys	Ile	Pro
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		195					200					205		Phe	
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Lys 225	Lys	Thr	Lys	Ile	Thr 230	Thr	Asp	Lys	Ile	Glu 235	Ile	Asn	Leu	Gly	Phe 240

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Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu 260 265 270

Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly 275 280 285

Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe 290 295 300

Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu 305 310 315 320

Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe 325 330 335

Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg 340 345 350

Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu 355 360 365

Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr 370 375 380

Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu 385 390 395 400

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Thr Phe Leu Leu Val Leu Ala Ser Glu Leu Tyr Phe Pro Ser Ser Ser 35 40 45

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Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe 65 70 75 80

Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu 85 90 95

Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr
100 105 110

Ser Pro Glu Ile Phe Glu Thr Ser Val Ile Cys Leu Phe Trp Leu Ser 115 120 125

Ala Asp Phe Ser Ser Leu Val Val Ser Leu Ser Gln His Pro Ala Glu 130 135 140

Ile Val Ala Ile Ala Glu Ser Gly Lys Thr Lys Pro Lys Pro Arg Asn 145 150 155 160

Leu Phe His Phe Ile Phe Phe Ile Val Val Leu Leu Ile Asn Cys
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- Asn Gly Lys Lys Tyr Ser Asp Leu Leu Ala Glu Lys Lys Val Ile Ile 145 150 155 160
 - Val Ala Val Asp Trp Asp Leu Ser Lys Glu Asp Lys Asp Leu Ile Lys

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 - Ile Ala Gly Tyr Ala Ser Ser Lys Phe Leu Ala Tyr Lys Phe Pro Asn 195 200 205
 - Asp Glu Ala Lys Arg Thr Ile Ala Pro Phe Gly Gly His Gly Ala 210 215 . 220
 - Gly Val Thr Asp Phe Ile Ala Gly Phe Leu Ala Gly Ile Ala Lys Tyr
 225 230 235 240
 - Asn Asn Asp Asn Pro Thr Ala Lys Val Thr Ile Ser Asp Asn Asn Ile
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 - Asn Ile Asp Thr Gly Phe Ile Ser Asn Asp Lys Thr Ala Thr Phe Ile 260 265 270
 - Asn Gly Ile Val Asn Lys Ser Ser Leu Val Leu Pro Val Ala Gly Ser 275 280 285
 - Leu Thr Ser Ser Val Val Asp Ala Ile Lys Lys Ser Asn Lys Asp Thr 290 295 300
 - Lys Tyr Leu Ile Gly Val Asp Thr Asp Gln Ser Lys Ile Phe Ser Pro 305 310 315 320
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 - Tyr Gln Val Leu Thr Asp Ile Trp Leu Lys Lys Glu Asp Ser Lys Phe 340 345 350
 - Leu Gly Ser Phe Arg Ser Phe Lys Leu Thr Asn Pro Ala Asn Ala Thr 355 360 365
 - Val Tyr Lys Gly Ile Ser Asp Asp Phe Val Gly Val Ser Asn Ser Thr 370 375 380

Val Ala Asp Ala Asp Lys Val Lys Ala Gln Glu Phe Leu Asn Glu Ala 385 390 395 400

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SEQUENCE LISTING

<110> King, Kendall W Madura, Rebecca A Rosey, Everett L

<120> NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA PNEUMONIAE mhp3 GENE AND USES THEREOF

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Ile Met Ala Ala Lys Ala Asp Ala Asn Lys His Phe Gly Leu Asn Met 65 70 75 80

Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn Ser Phe Asn Gln \$85\$

Ser Ser Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu Thr Gly Glu 100 105 110

Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu Ser Gly Phe Gln 130 135 140

His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro Glu Asn Lys Gln 145 150 155 160

Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile Asp Trp Thr Asp 165 170 175

Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn Leu Thr Tyr Lys 180 185 190

Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn Ala Ser Phe Leu 195 200 205

Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser Ala Ile Val Ile 210 215 220

Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile Ala Gly Tyr Leu 225 230 235 240

Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp Lys Lys Thr Lys 245 250 255

Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe Asp Val Gln Asp 260 265 270

Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser Lys Asp Lys Pro 275 280 285

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Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu 65 70 75 80

Thr Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu 85 90 95

Gly Lys Tyr Ser Ser Leu Ala Asn Thr Asn Lys Asn Val Trp Val Leu 100 105 110

Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro 115 120 125

Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile 130 135 140

Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn 145 150 155 160

Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn 165 170 175

Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser 180 185 190

Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile 195 200 205

Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp 210 215 220

Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe 225 230 235 240

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185

180

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22

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360

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Gly Leu Asn Met Ala Ile Val Thr Ala Gly Gly Thr Val Asn Asp Asn 50 55 60 -

Ser Phe Asn Gln Ser Gly Trp Glu Ala Ile Gln Gln Leu Gly Ala Leu 65 70 75 80

Thr Gly Glu Ile Thr Ser Val Asp Ser Ser Thr Ala Glu Leu Glu 85 90 95

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Ser Gly Phe Gln His Gly Asp Ala Phe Thr Arg Trp Leu Lys Ile Pro 115 120 125

Glu Asn Lys Gln Leu Phe Thr Glu Lys Asn Ile Ile Ile Leu Gly Ile 130 135 140

Asp Trp Thr Asp Thr Glu Asn Val Ile Pro Thr Gly Arg Tyr Ile Asn 145 150 155

Leu Thr Tyr Lys Thr Glu Glu Ala Gly Trp Leu Ala Gly Tyr Ala Asn 165 170 175

Ala Ser Phe Leu Ala Lys Lys Phe Pro Ser Asp Pro Thr Lys Arg Ser 180 185 190

Ala Ile Val Ile Gly Gly Gly Ile Ser Pro Ala Val Thr Asp Phe Ile 195 200 205

Ala Gly Tyr Leu Ala Gly Ile Lys Ala Trp Asn Leu Lys Asn Ser Asp 210 215 220

Lys Lys Thr Lys Ile Thr Thr Asp Lys Ile Glu Ile Asn Leu Gly Phe 225 230 235

Asp Val Gln Asp Thr Ser Thr Lys Glu Arg Leu Glu Gln Ile Ala Ser 245 250 255

Lys Asp Lys Pro Ser Thr Leu Leu Ala Val Ala Gly Pro Leu Thr Glu 260 265 Ile Phe Ser Asp Ile Ile Ala Asn Gln Asn Asp Arg Tyr Leu Ile Gly 280 285 Val Asp Thr Asp Gln Ser Leu Val Tyr Thr Lys Thr Lys Asn Lys Phe 295 Phe Thr Ser Ile Leu Lys Asn Leu Gly Tyr Ser Val Phe Ser Val Leu 305 310 315 Ser Asp Leu Tyr Thr Lys Lys Ser Asn Ser Arg Asn Leu Ala Gly Phe 325 330 335 Glu Phe Gly Lys Lys Ser Ala Thr Val Tyr Leu Gly Ile Lys Asp Arg 340 345 350 Phe Val Asp Ile Ala Asp Thr Ser Leu Glu Gly Asn Asp Lys Lys Leu 355 360 Ala Thr Glu Ala Ile Ser Glu Ala Lys Lys Glu Phe Glu Glu Lys Thr 375 Lys Thr Ile Pro Ala Glu Glu Val Arg Lys Thr Leu Glu Ile Pro Glu 385 390 395 Met Pro Asp Lys Gln Pro Asp Lys Gln Gln Glu Ser Leu Asp Lys Leu 405 410 Xaa Xaa Xaa Xaa Xaa Xaa 420 <210> 5 <211> 602 <212> DNA <213> Mycoplasma hyopneumoniae <400> 5 atgataatat ttttttcagt aaataattgc ttattttcag ggatttttaa tcatcttgtg aacgcatcac cgtgttgaaa accagaaagt actcaaacat ttttgttggt attagcaagt 120 gagctatatt ttccttcaag ttcagcagtt gaactatcta ctgaagtaat ctcacctcca 180

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Ser Cys Trp Ile Ala Ser Gln Leu Asp Trp Leu Asn Glu Leu Ser Phe 65 70

Thr Val Pro Pro Ala Val Thr Ile Ala Ile Phe Ser Pro Lys Cys Leu 85 95

Phe Ala Ser Ala Phe Ala Ala Ile Ile Ser Asp Phe Arg Ser Leu Thr 100 105

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tgta attggcataa aaactgcc	28		
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atgg aataaatttc ttgg	24		
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Asp Arg Val Ser Gln Glu Thr Asn Asn Gln Ser Glu Leu Ile Gly Lys 100 105 110

Tyr Lys Asn Phe Leu Asn Gly Asn Lys Asn Val Trp Ile Leu Thr Gly 115 120 125

Phe Gln Gln Gly Gln Glu Phe Pro Lys Phe Leu Lys Gln Thr Asp Ser 130 135 140

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Val Ala Val Asp Trp Asp Leu Ser Lys Glu Asp Lys Asp Leu Ile Lys 165 170 175

Ala Gly His Phe Ile Ser Leu Leu Tyr Lys Thr Glu Glu Ala Gly Phe 180 185 190

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Gly Val Thr Asp Phe Ile Ala Gly Phe Leu Ala Gly Ile Ala Lys Tyr 225 230 235 240

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Lys Tyr Leu Ile Gly Val Asp Thr Asp Gln Ser Lys Ile Phe Ser Pro 305 310 315

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Leu Gly Ser Phe Arg Ser Phe Lys Leu Thr Asn Pro Ala Asn Ala Thr 355 360 365

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